Page 1 of 8



PCT09

RAW SEQUENCE LISTING DATE: 06/12/2002 PATENT APPLICATION: US/09/744,100B TIME: 14:37:31

Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\1744100B.raw

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```
<110> APPLICANT: Cahoon, Rebecca
            Gutteridge, Steven
            Lee, Jian-Ming
   . 6
            McGonigle, Brian
   - 7
            Rafalski, Antoni
    9 <120> TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
   11 <130> FILE REFERENCE: BB-1174
   13 <140> CURRENT APPLICATION NUMBER: 09/744,100B
--> 14 <141> CURRENT FILING DATE: 2002-04-04
   16 <150> PRIOR APPLICATION NUMBER: PCT/US99/15931
   17 <151> PRIOR FILING DATE: 1999-07-14
   19 <150> PRIOR APPLICATION NUMBER: 60/093,209
   20 <151> PRIOR FILING DATE: 1998-07-17
   22 <160> NUMBER OF SEQ ID NOS: 12
   24 <170> SOFTWARE: Microsoft Office 97
   26 <210> SEQ ID NO: 1
   27 <211> LENGTH: 1201
   28 <212> TYPE: DNA
   29 <213> ORGANISM: Zea mays
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**ENTERED** 

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33 caactegete ettecagtee cateceegee geegteggge cetactetea getecaacea
34 tgcaageece ettgeegeee etaettgeeg tegeageege etcegeatet eegeeacate
                                                                      180
35 cacggctgcg cogteteett cgtcggctgc cgctgccacc gcgtcgctga gtcgagtgga
36 cgtgctctcg gaggcgctcc cttttattca gcgattcaaa ggcaagacgg tggtggtcaa
37 gtacggcggt gcggcgatga agtccccgga gctgcaggcg tccgtgatcc gcgatctcgt
38 getgetetee tgegteggee teegceeegt gettgtteae ggeggeggte eggagattaa
39 tteetggetg etgegeteg gegtegagee geagtteege gaeggeetee gegteaegga
40 cgcgctcacc atggaggtcg tcgagatggt gctagtcggg aaggtcaaca aaaaccttgt
41 ttccctcatc aacatcgcgg gaggcaccgc cattggtctg tgcggcaagg acgcgcgcct
42 tatcaccgct cgcccgtctc caaatgcagc ggcgctggga ttcgtcggcg aggtttcgcg
43 cgtggacgcc accgtcctcc atcccatcat cgccgcgggc catatcccgg ttatcgccac
                                                                      720
44 cgttgccgcc gacgagactg ggcaagccta taacatcaat gctgatacgg cggctggcga
45 gattgccgct gccgtgggcg ccgagaagct gctgttgctc acagatgtgt ctggcatttt
                                                                      840
46 ggcggaccgt aatgaccctg ggagcctggt gaaggtggtc gacattgctg gggtgcggaa
47 gatggtggct gacgggaagg tagctggtgg gatgataccc aaggtggagt gttgtgttca
48 cgcccttgca caaggtgtac acaccgcaag tatcattgat gggcgtgttc cacactctct 1020
49 totgottgag attotoacag acgagggoac aggoaccatg atcactggot gagotgotto 1080
50 atgeetteat ggtattttee tgtgeetett tteteatatt gttgtgtttt atggetatgt 1140
51 agactaaact caagattgca ataagactac ctaagtttgg ttgaaaaaaa aaaaaaaaa 1200
52 a
54 <210> SEQ ID NO: 2
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55 <211> LENGTH: 345

Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\I744100B.raw

56 <212> TYPE: PRT 57 <213> ORGANISM: Zea mays 59 <400> SEQUENCE: 2 60 Met Leu Leu Thr Lys Pro Tyr Leu Ser Asn Ser Leu Leu Pro Val Pro 10 63 Ser Pro Pro Pro Ser Gly Pro Thr Leu Ser Ser Asn His Ala Ser Pro 20 25 66 Leu Ala Ala Pro Thr Cys Arg Arg Ser Arg Leu Arg Ile Ser Ala Thr 35 40 69 Ser Thr Ala Ala Pro Ser Pro Ser Ser Ala Ala Ala Thr Ala Ser 55 72 Leu Ser Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg. 70 75 Phe Lys Gly Lys Thr Val Val Lys Tyr Gly Gly Ala Ala Met Lys 90 85 78 Ser Pro Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser 81 Cys Val Gly Leu Arg Pro Val Leu Val His Gly Gly Pro Glu Ile 115 120 84 Asn Ser Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asp Gly 130 135 140 87 Leu Arg Val Thr Asp Ala Leu Thr Met Glu Val Val Glu Met Val Leu 155 150 90 Val Gly Lys Val Asn Lys Asn Leu Val Ser Leu Ile Asn Ile Ala Gly 165 170 93 Gly Thr Ala Ile Gly Leu Cys Gly Lys Asp Ala Arg Leu Ile Thr Ala 180 185 96 Arg Pro Ser Pro Asn Ala Ala Leu Gly Phe Val Gly Glu Val Ser 195 200 99 Arg Val Asp Ala Thr Val Leu His Pro Ile Ile Ala Ala Gly His Ile 215 220 102 Pro Val Ile Ala Thr Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn 230 235 105 Ile Asn Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala 245 250 108 Glu Lys Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg 260 265 111 Asn Asp Pro Gly Ser Leu Val Lys Val Val Asp Ile Ala Gly Val Arg 280 114 Lys Met Val Ala Asp Gly Lys Val Ala Gly Gly Met Ile Pro Lys Val 295 290 117 Glu Cys Cys Val His Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile 310 315 120 Ile Asp Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp 330 325 123 Glu Gly Thr Gly Thr Met Ile Thr Gly 340 126 <210> SEQ ID NO: 3 127 <211> LENGTH: 1186

Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\I744100B.raw

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128 <212> TYPE: DNA
  129 <213> ORGANISM: Oryza sativa
  131 <220> FEATURE:
  132 <221> NAME/KEY: unsure
  133 <222> LOCATION: (613)
  134 <223> OTHER INFORMATION: n = A, C, G, or T
  136 <400> SEQUENCE: 3
  137 gcacgagtac agegeegeeg eegeegeeat geteetegeg aageeeeace teteeteete
  138 ctctttcctc ccatccacgc gggtgtctag ccccgctccg ggtcccaacc acgcaaagcc
                                                                       120
  139 categorge teteorgec etegacgetg ceteogtete geogteacat ecgeogoge
  140 geoggetget tegteggegg aggeggegge ggegetgage egegtggatg tgeteteaga
  141 ggcgctcccc ttcatccagc gcttcaaggg gaagaccgtg gtggtgaagt acggcggcgc
  142 ggcgatgaag tcgccggagc tccaggcttc agtgatccgc gacctggtcc tcctctcgtg
                                                                       360
  143 cgtcggcctc caccccgtgc tcgtccacgg cggcgggccc gagatcaact cctggctgct
                                                                       420
  144 ccqcqtcqqc qtcqaqccqc aqttccqqaa cgqcctccqc qtcactqacq cqctcaacat
                                                                       480
  145 ggaggtegte gagatggtge tegteegcaa ggteaacaaa gaacteetet eeetcateaa
                                                                       540
                                                                       600
  146 actecegggg gggagegeeg taagtetetg ttggaaggaa getegeetee teaacgageg
147 gccctccccg aangaaaagg gccttcggtt tgtcggcggg gtctggcgcg tggacgccac
                                                                       660
  148 egicetecae ecaateateg eeteeggica cateeeggic ategeeactg tgggegeega
  149 cgagaccggg caggcctaca acatcaacgc tgacacggcg gccggcgaga tcgccgccgc
  150 ggtcggcgcg gagaagctgt tgctgctcac agatgtgtct ggaattctgg ccgaccgtaa
                                                                       840
  151 tgaccccggg agtctggtga aagagatcga cattgctggg gtgcggcaga tggtggccga
                                                                       900
  152 cgggcaggta gctggtggga tgataccgaa ggtggaatgc tgcgtgcgtg ccctcgcaca 960
  153 gggcgtgcac actgcaagca tcatcgatgg gcgtgtcccg cactcgttgc tgctcgagat 1020
  154 teteacagat gagggeactg geactatgat caetggetga ggtgatteat eccgtegtgg 1080
  155 tatteteegg tgeetetett eteataetgt aatgtaattt geatttgata tgeeteatga 1140
  158 <210> SEQ ID NO: 4
  159 <211> LENGTH: 343
  160 <212> TYPE: PRT
 161 <213> ORGANISM: Oryza sativa
  163 <220> FEATURE:
  164 <221> NAME/KEY: UNSURE
 165 <222> LOCATION: (195)
  166 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID
  168 <400> SEQUENCE: 4
 169 Met Leu Leu Ala Lys Pro His Leu Ser Ser Ser Phe Leu Pro Ser
 170
                                          10
 172 Thr Arg Val Ser Ser Pro Ala Pro Gly Pro Asn His Ala Lys Pro Ile
                  20
                                      25
                                                          30
 175 Ala Ala Ser Pro Ala Pro Arg Arg Cys Leu Arg Leu Ala Val Thr Ser
 176
 178 Ala Ala Ala Pro Ala Ala Ser Ser Ala Glu Ala Ala Ala Leu Ser
 179
                              55
 181 Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys
 182 65
                          70
                                              75
 184 Gly Lys Thr Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro
                      85
                                          90
 187 Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val
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Input Set: A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\1744100B.raw

```
188
                     100
                                         105
    190 Gly Leu His Pro Val Leu Val His Gly Gly Pro Glu Ile Asn Ser
                                     120
                                                         125
                115
    193 Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asn Gly Leu Arg
            130
                                 135
                                                     140
    196 Val Thr Asp Ala Leu Asn Met Glu Val Val Glu Met Val Leu Val Arg
    197 145
                             150
                                                 155
    199 Lys Val Asn Lys Glu Leu Leu Ser Leu Ile Lys Leu Pro Gly Gly Ser
                                             170
                         165
    202 Ala Val Ser Leu Cys Trp Lys Glu Ala Arg Leu Leu Asn Glu Arg Pro
    203
                     180
                                         185
M_{i}/_{	au}> 205 Ser Pro Xaa Glu Lys Gly Leu Arg Phe Val Gly Gly Val Trp Arg Val
    206
                 195
                                     200
    208 Asp Ala Thr Val Leu His Pro Ile Ile Ala Ser Gly His Ile Pro Val
    209
            210
                                                     220
                                 215
    211 Ile Ala Thr Val Gly Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn
                                                 235
                             230
    214 Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala Glu Lys
    215
                         245
                                             250
    217 Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp
    218
                    260
                                         265
    220 Pro Gly Ser Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met
                275
                                     280
                                                         285
    223 Val Ala Asp Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys
                                 295
    226 Cys Val Arg Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp
    227 305
                             310
                                                 315
    229 Gly Arg Val Pro His Ser Leu Leu Glu Ile Leu Thr Asp Glu Gly
    230
                         325
                                             330
    232 Thr Gly Thr Met Ile Thr Gly
    233
                     340
    235 <210> SEQ ID NO: 5
    236 <211> LENGTH: 1204
    237 <212> TYPE: DNA
    238 <213> ORGANISM: Glycine max
    240 <400> SEQUENCE: 5
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    241 geacgagatg atggeaggtg cagecaaaac cetaaceaat etttgeecet ettteeeatt
    242 cccaaccaaa ccccaaaacc aactcaccac tagccacget ttecetteca ctcgcetecg
                                                                             120
    243 ccaccgcgcc atttccgcgg tggcgaacgc ggcgcaacct ccactcgccg ccgccactgc
    244 caccaggat caqtaccagg tegatatet ctegagteg eteceettea tecagaaatt
    245 ccqcqqcaaa accatcqtcq tcaaqtacqq cqqcqqccqcc atgaaqtccc cqgagctcca
    246 ggcctccqtq atcaacqacc ttqtcctcct ctcctqcqtc qqcctccqcc ccgtcctggt
                                                                             360
    247 ccacggcggc ggccccgaga tcaactcctg gctcggccgc ctcaacatcc ccgccgtctt
                                                                             420
    248 ccgcgacggc ctccgcgtca ccgacgccga caccatggag atcgtctcca tggtcctcgt
                                                                             480
    249 cggaaaagtc aacaaaaccc tagtttctct aattaacaag gccggcgcca ccgccgtcgg
                                                                             540
    250 cetetetgge atggaeggee geeteeteac egeeegeeee geteecaagg eegeegaeet
                                                                             600
    251 cggctacgtc ggcgaggtcg cacgcgtcga tcccgccgtc ctccgctccc taatcgacac
    252 cagccacate ecceptegtea ecteegtege egeogatgaa teeggacage ectacaacat
    253 caacgccgac accgtcgccg gagaattggc agcgtcgctc ggcgcggaga agctgattct
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Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\I744100B.raw

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254 gctgaccgat gtggcgggaa ttctggaaga tcggaacgac cctgacagct tggtgaagaa
255 gattgacata aaaggagtga agaaaatgat ggaagatgga aaagttggtg gtggaatgat
256 acctaaggtt aattgttgcg ttaggtcctt ggcgcaaggg gttattacag cgagtattat
257 tgatggtagg gttccgcatt ctttgttgct tgagattttg actgatgaag gtgctggaac 1020
258 tatgataact ggataagttt atttatttat ggtgtttgga ttttttcttt tcaatcaagc 1080
259 cttgagttga ggttgcattg cagcacttgt tttgttagag attggtgatt gtttttaagt 1140
261 aaaa
263 <210> SEQ ID NO: 6
264 <211> LENGTH: 342
265 <212> TYPE: PRT
266 <213> ORGANISM: Glycine max
268 <400> SEQUENCE: 6
269 Met Met Ala Gly Ala Ala Lys Thr Leu Thr Asn Leu Cys Pro Ser Phe
270
                                        10
272 Pro Phe Pro Thr Lys Pro Gln Asn Gln Leu Thr Thr Ser His Ala Phe
275 Pro Ser Thr Arg Leu Arg His Arg Ala Ile Ser Ala Val Ala Asn Ala
             35
                                40
278 Ala Gln Pro Pro Leu Ala Ala Thr Ala Thr Glu Gly Gln Tyr Arg
279
281 Val Asp Val Leu Ser Glu Ser Leu Pro Phe Ile Gln Lys Phe Arg Gly
282
                        70
                                            75
284 Lys Thr Ile Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu
287 Leu Gln Ala Ser Val Ile Asn Asp Leu Val Leu Leu Ser Cys Val Gly
288
               100
                                   105
290 Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp
291
           115
                               120
293 Leu Gly Arg Leu Asn Ile Pro Ala Val Phe Arg Asp Gly Leu Arg Val
                           135
                                               140
296 Thr Asp Ala Asp Thr Met Glu Ile Val Ser Met Val Leu Val Gly Lys
                       150
                                           155
299 Val Asn Lys Thr Leu Val Ser Leu Ile Asn Lys Ala Gly Ala Thr Ala
                   165
                                       170
302 Val Gly Leu Ser Gly Met Asp Gly Arg Leu Leu Thr Ala Arg Pro Ala
303
               180
                                   185
305 Pro Lys Ala Ala Asp Leu Gly Tyr Val Gly Glu Val Ala Arg Val Asp
                               200
308 Pro Ala Val Leu Arg Ser Leu Ile Asp Thr Ser His Ile Pro Val Val
                           215
311 Thr Ser Val Ala Ala Asp Glu Ser Gly Gln Pro Tyr Asn Ile Asn Ala
312 225
314 Asp Thr Val Ala Gly Glu Leu Ala Ala Ser Leu Gly Ala Glu Lys Leu
315
                   245
                                       250
317 Ile Leu Leu Thr Asp Val Ala Gly Ile Leu Glu Asp Arg Asn Asp Pro
                                   265
               260
320 Asp Ser Leu Val Lys Lys Ile Asp Ile Lys Gly Val Lys Lys Met Met
321
           275
                               280
```

RAW SEQUENCE LISTING ERROR SUMMARY

PATENT APPLICATION: US/09/744,100B

TIME: 14:37:32

Input Set : A:\BB1174 US PCT seqlist01.txt
Output Set: N:\CRF3\06122002\I744100B.raw

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 613 Seq#:4; Xaa Pos. 195 Seq#:7; N Pos. 492,493,494,495,496,497,498,499,500,501,502,503,504,505,506 Seq#:7; N Pos. 507,508,509,510,511,512,513,514,515,516,517,518,519,520,521 Seq#:7; N Pos. 522,523,524,525,526,527,528,529,530,531,532,533,534,535,536 Seq#:7; N Pos. 537,538,539,540,541,542 Seq#:8; Xaa Pos. 133,144,145,146,147,148,149,150,151,152,153,154,155,156 Seq#:8; Xaa Pos. 157,158,159,160 Seq#:12; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,24 Seq#:12; Xaa Pos. 25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43 Seq#:12; Xaa Pos. 44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,60,61,63,64 Seq#:12; Xaa Pos. 65,66,67,75,81,83,87,107,118,134,136,137,138,139,140,141 Seq#:12; Xaa Pos. 144,152,153,156,158,163,168,170,174,175,176,178,179,181 Seq#:12; Xaa Pos. 182,184,185,186,187,188,191,192,193,196,198,199,200,201 Seq#:12; Xaa Pos. 203,204,207,209,211,212,213,214,217,218,219,221,222,223 Seq#:12; Xaa Pos. 228,229,230,232,236,239,247,251,254,255,261,263,267,271 Seq#:12; Xaa Pos. 274,277,282,283,286,290,292,293,294,296,298,306,310,311 Seq#:12; Xaa Pos. 317,340